

L. Helms

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Attorney
PAID

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/250,056A

DATE: 09/28/1999
TIME: 14:59:56

Input Set: I250056A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Marks, James D
2 Poul, Marie A
3 <120> TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
4 <130> FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab
5 <140> CURRENT APPLICATION NUMBER: US/09/250,056A
6 <141> CURRENT FILING DATE: 1999-02-12
7 <150> EARLIER APPLICATION NUMBER: 60/082,953
8 <151> EARLIER FILING DATE: 1998-04-24
9 <160> NUMBER OF SEQ ID NOS: 4
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 246
13 <212> TYPE: PRT
14 <213> ORGANISM: Artificial Sequence
15 <220> FEATURE:
16 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv F5 amino
17 acid sequence
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19 <221> NAME/KEY: DOMAIN
20 <222> LOCATION: (31)..(35)
21 <223> OTHER INFORMATION: VH-CDR1
22 <220> FEATURE:
23 <221> NAME/KEY: DOMAIN
24 <222> LOCATION: (50)..(66)
25 <223> OTHER INFORMATION: VH-CDR2
26 <220> FEATURE:
27 <221> NAME/KEY: DOMAIN
28 <222> LOCATION: (99)..(108)
29 <223> OTHER INFORMATION: VH-CDR3
30 <220> FEATURE:
31 <221> NAME/KEY: DOMAIN
32 <222> LOCATION: (157)..(170)
33 <223> OTHER INFORMATION: VL-CDR1
34 <220> FEATURE:
35 <221> NAME/KEY: DOMAIN
36 <222> LOCATION: (186)..(192)
37 <223> OTHER INFORMATION: VL-CDR2
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40 <222> LOCATION: (225)..(235)
41 <223> OTHER INFORMATION: VL-CDR3
42 <400> SEQUENCE: 1
43 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
44 1 5 10 15

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/250,056A

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TIME: 14:59:56

Input Set: I250056A.RAW

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45      Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
46              20                      25                      30
47      Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
48              35                      40                      45
49      Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val
50              50                      55                      60
51      Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
52              65                      70                      75                      80
53      Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
54              85                      90                      95
55      Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly
56              100                     105                     110
57      Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
58              115                     120                     125
59      Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
60              130                     135                     140
61      Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
62      145                     150                     155                     160
63      Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro
64              165                     170                     175
65      Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser
66              180                     185                     190
67      Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser
68              195                     200                     205
69      Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
70              210                     215                     220
71      Gln Phe Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr
72      225                     230                     235                     240
73      Lys Leu Thr Val Leu Gly
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75 <210> SEQ ID NO 2

76 <211> LENGTH: 242

77 <212> TYPE: PRT

78 <213> ORGANISM: Artificial Sequence

79 <220> FEATURE:

80 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
81 acid sequence

82 <220> FEATURE:

83 <221> NAME/KEY: DOMAIN

84 <222> LOCATION: (31)..(35)

85 <223> OTHER INFORMATION: VH-CDR1

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89 <223> OTHER INFORMATION: VH-CDR2

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91 <221> NAME/KEY: DOMAIN

92 <222> LOCATION: (99)..(108)

93 <223> OTHER INFORMATION: VH-CDR3

94 <220> FEATURE:

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/250,056A

DATE: 09/28/1999
TIME: 14:59:56

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95 <221> NAME/KEY: DOMAIN
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110             20             25             30
111   Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
112             35             40             45
113   Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
114             50             55             60
115   Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
116             65             70             75             80
117   Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
118             85             90             95
119   Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly
120             100            105            110
121   Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
122             115            120            125
123   Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
124             130            135            140
125   Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
126             145            150            155            160
127   Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
128             165            170            175
129   Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
130             180            185            190
131   Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
132             195            200            205
133   Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
134             210            215            220
135   Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
136             225            230            235            240
137   Lys Arg
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139 <211> LENGTH: 738
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleic acid
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PAGE: 4

RAW SEQUENCE LISTING PATENT APPLICATION US/09/250,056A

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TIME: 14:59:56

Input Set: I250056A.RAW

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145 <400> SEQUENCE: 3
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148   ccaggaagg ggctggagt ggtctcagct attagtgggtc gtggtgataa cacatactac 180
149   gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
150   ctgcaaatac acagcctgag agccgaggac acggccgttt attactgtgc gaaaatgaca 300
151   agtaacgcgt tcgcatttga ctactggggc caggaacccc tggtcaccgt ctccctcagg 360
152   ggaggcgggt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag 420
153   ccgccctcag tgtctggggc ccagggcag agggtcacca tctcctgcac tgggagcagc 480
154   tccaacatcg gggcaggtta tgggtgtacac tggtagcagc agcttccagg aacagccccc 540
155   aaactcctca tctatggtaa caccaatcgg cctcagggg tccctgaccg attctctggc 600
156   ttcaagtctg gcacctcagc ctccctggcc atcactgggc tccaggctga ggatagggt 660
157   gattattact gccagttcta tgacagcagc ctgagtgggt ggggtgttcg cggaggggacc 720
158   aagctgaccg tgctaggt                                     738
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160 <211> LENGTH: 726
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
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166 <220> FEATURE:
167 <221> NAME/KEY: modified_base
168 <222> LOCATION: (111)
169 <223> OTHER INFORMATION: N = A, C, G, OR T
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173   ccaggaagg ggctggagt ggtctcatca attagtggca gtagtagata catatattac 180
174   gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
175   ctgcaaatac acagcctgcg agccgaggac acggccgttt attactgtgc gaaaatggat 300
176   gcttcgggga gttattttaa tttctggggc cagggcacc c tggtcaccgt ctccctcagg 360
177   ggaggcgggt caggcggagg tggctctggc ggtggcggat cggaaacgac actcacgcag 420
178   tctccatcct tcctgtctgc attttagtaga gacagaatca ccatcacttg ccgggccagt 480
179   ccgggcatta ggaattattt agcctgggtat cagcaaaaac cagggaaagc ccctaagctc 540
180   ctgatctatg ctgcattctac tttgcaaagt ggggtcccat caaggttcag cggcagtggg 600
181   tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660
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183   aaacgt                                     726

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w--OK

PAGE: 5

VERIFICATION SUMMARY
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DATE: 09/28/1999
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